

### **AMENDMENTS TO THE SPECIFICATION**

Please amend the specification as follows:

Please replace the first paragraph on page 19, lines 1-8, with the following amended paragraph:

Figure 1: Multiple sequence alignment calculated with the program ClustalW of mevalonate kinase sequences from mouse (SEQ ID NO: 3), rat (SEQ ID NO: 4), man (SEQ ID NO: 2), yeast (SEQ ID NO: 6), *Arabidopsis thaliana* (ARATH) (SEQ ID NO: 5), *Schizosaccharomyces pombe* (SCHPO) (SEQ ID NO: 7), *Pyrococcus abyssi* (PYRAB) (SEQ ID NO: 8), *Pyrococcus horikoshii* (PYRHO) (SEQ ID NO: 9), *Pyrococcus furiosus* (PYRFU) (SEQ ID NO: 10), *Methanobacterium thermoautotrophicum* (METTH) (SEQ ID NO: 11), *Archaeoglobus fulgidus* (ARCFU) (SEQ ID NO: 12), *Methanococcus jannaschii* (METJA) (SEQ ID NO: 13), *Aeropyrum pernix* (AERPE) (SEQ ID NO: 14), and *Paracoccus zeaxanthinifaciens* (PARACOCUS) (SEQ ID NO: 1). Numbering is according to the amino acid sequence of *Paracoccus zeaxanthinifaciens* mevalonate kinase.